



Supplementary Figure 1:

359 sequences positive for the pan-*Chlamydiales* qPCR were plotted according to the Best Blast identity with closest reference 16S rRNA gene. According to the cut-off currently used for the taxonomic *Chlamydiales* classification (2, 3), we could obtain an insight of the taxonomic classification of the *Chlamydiales* DNA at the species level (97%), at the genus level (95%) and at the family level (90%). Please note that when several samples exhibit the same percentage of identity with the closest 16S rRNA gene, they are all plotted as individual point on the same horizontal line.

References cited:

2. **Everett KD, Bush RM, Andersen AA.** 1999. Emended description of the order Chlamydiales, proposal of Parachlamydiaceae fam. nov. and Simkaniaceae fam. nov., each containing one monotypic genus, revised taxonomy of the family Chlamydiaceae, including a new genus and five new species, and standards for the identification of organisms. *Int J Syst Bacteriol* **49 Pt 2**:415–440.
3. **Greub G.** 2010. International Committee on Systematics of Prokaryotes * Subcommittee on the taxonomy of the Chlamydiae: Minutes of the inaugural closed meeting, 21 March 2009, Little Rock, AR, USA. *Int J Syst Evol Microbiol* **60**:2691–2693.